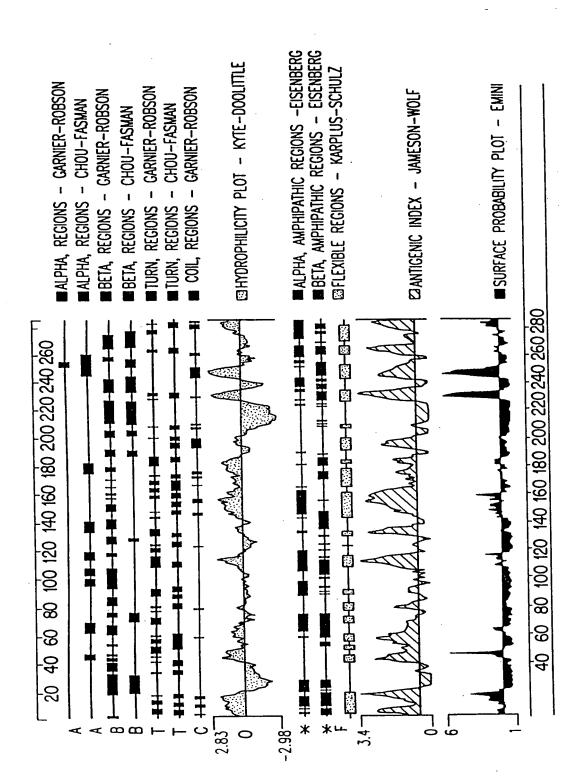
50 10 30 90 110 70 CTGAGCCCCTCTCTGCTGCCAGACACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCT 170 150 130 GAGGCACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCC 230 190 210 ACAGCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCC 290 250 270 GAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGG P P G D W G P P P W 330 350 310 AGATCCACCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCC 410 390 370 CCCTGCTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAG PVGSE CKED Р S F 470 450 430 TGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGC RVKΕ C Ε PKC 530 490 510 ACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG TY GL G Ι C E 590 570 550 TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCC A M GS R QCQM 650 630 610 AGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGG SPGG С ENAV 710 690 670 GACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG RVOKA T S H C A A C R Α Υ S 770 750 730 GGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCC C Q N CP G Τ F TESQ 830 810 790 · QTKC ٧ $\mathsf{T}^{\mathsf{K}} \mathsf{K}^{\mathsf{A}}$ NGTLEEC Q Н S 890 870 850 GGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATC H <u>W V W W</u> F S SS

930 950 910 GTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAGAAAGCCAAGGGGT IICVKRRKPRG 990 1010 970 GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCC SVQRKRQE A E G E AK V T V 1050 1070 1030 ACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACA IEALQAPPDVTT AVEET 1110 1130 1090 ATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGC SPNH* S F T G R 1190 1170 1150 CAGAGATACCTGGAGCGACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGA 1230 1250 1290 1310 GTGGCGCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAG 1370 1350 1330 GGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCA 1430 1410 GTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAGAGGGCCTTCA 1490 1470 1450 GACCCCAGCTGTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTG 1530 1570 1590 1610 GAAGTGATTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAG 1670 1650 1630 1690 ΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑΑ

FIG.1B

1	MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVG	50
1	: .: .::: :MVSLPRLCALWGCLLTAVHLGQCVTCSDKQYLHD	34
51	SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD	100
35	:: . : . . .: :: : : : GQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE	84
101	PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRV	150
85	131
151	QKGGTESQDTLCQNCPPGTFSPNGTL.EECQHQTKC.SWLVTKAGAGTSS	198
132	. : . : : . .:. . . . : MEMATETTDTVCHPCPCGFFSNQSSLFEKCYPNTSCEDKNLEVLQKGTSQ	181
199	SHWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIV	239
182	TNVICGLKSRMRALLVIPVVMGILITIFGVFLYIKKVVKKPKDNEMLPPA	231
240	SVQRKRQEAEGEATVIEALQAPPDVTTVAVEETIPSFTGRSPNH	283
232	: . . :: . . : ARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQVTD	281

FIG.2



F16.3

30 50 10 CCCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGGAGAACTCGCCCCTC 70 90 110 CCATCGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCC 170 130 150 TCAGGCAGCGCCACCTGTGTCGCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTC 210 230 190 TGCTGCCAGACACCCCCTGCTGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTT 290 250 270 GTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTCTGGCCCACAGCCGCAGCA 310 330 350 ATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTC 370 390 410 TGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCC P G D W G 450 470 430 AGAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCC 490 510 530 CCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAG EDEYP S E C ALPSCK ٧ G 570 590 550 TGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAA KEACGE Т GTVCE Y R V 630 650 610 CCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGC S K C AHLN G 670 690 710 CAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTCAGGGGAAGAGGTCACCTGGAG C DG S P C D GRGH 770 750 730 GCTGGTGCCCACCTGAGTCCAGGCAGACAGAAAGGGGAACCAGACCCAGAGGTGGCCTTT R 0 K G Ε AHLG 830 810 790 GAGTCACTGAGCGCAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCAT Ε L LSAE A A N890 850 870 ARL S S A P CGQA G H L R 930 950 910 GCTGACGGCACACCTGGGGGCAGGGCCTGAGCCTACAGGGAGGCACAGGGCAGGTGGGCT ADGTPGGRA*

FIG.4A

GAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCA

2230	2250	2270
CCCCGACGCCAGAGATACCT	GGAGAGACGGCTGCTG	ATAGAGGCTGTCCACCTGGCGAAA
2290	2310	2330
CCACCGGAGCCCGGAGGCTT	GGGGGCTCCGCCCTGG	GCTGGTTTCCGTCTCCTCCAGTGG
2350	2370	2390
AGGGAGAGGTGGTGCCCCTG	CTGGTGGTAGAGCTGG	GGACGCCACGTGCCATTCCCATGG
2410	2430	2450
TTCAGTGAGGGGCTGGTGGC	CCTCTGTTCTGCTGTGG	CCTGAGCTCCCCAGAGTCCTGAGG
2470	2490	2510
AGGAGCCCCAGTTGCCCCTC	CGCTCACAGACCACACA	CCCAGCCCTCCTGGGCCAACCCAG
2530	2550	2570
AGGCCCCTTCAGACCCCAG(CTGTCTGCGCGTCTGAC	TCTTGTGGCCTCAGCAGGACAGGC
2590	2610	2630
CCCGGGCACTGCCTCACAG	CCAAGGCTGGAATGGGT	TGGCTGCAGTGTGGTGTTTAGTGG
2650	2670	2690
ATACCACATCGGAAGTGAT	FTTCTAAAAATTGGATT	TGAATTCGGAAAAAAA

FIG.4C

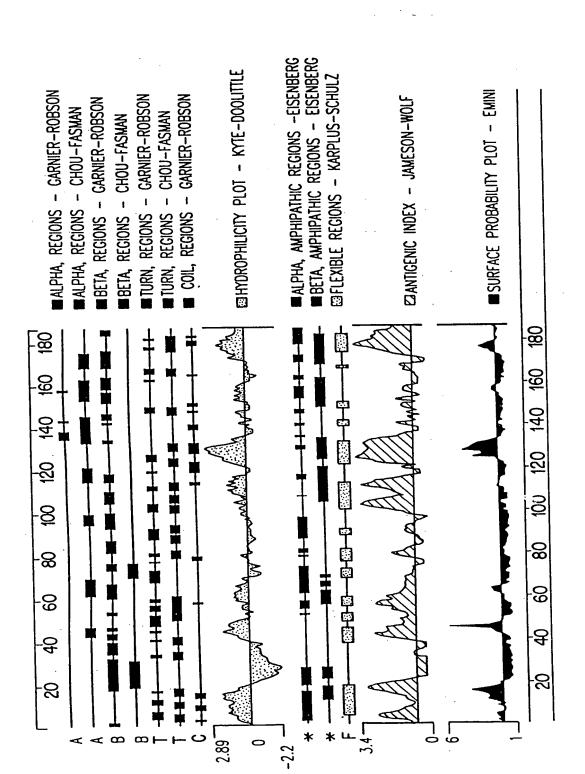
1	MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYP	48
1	MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQ	48
49	VGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQM .: . :. : :. .: :	98
49		98
99		133
99	:.::: :.:: :: :. .: ::: :: RCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFG	148
134	VAFESLSAEPVHAANGS	150
149	: .: .: . : . VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA	198
151	VPLEPHARLSMASAPCGQAGLHLRDRADGTPGGRA	185
199	: :	248

FIG.5

Sheet 9 of 31

Appl. No. 09/340,690; Group Art Unit: 1647 Dkt. No. 1488.0770007/EKS/PAJ; Batch No.: N/A Inventor(s): Ni et al.; Tel: 202/371-2600

Title: Human Tumor Necrosis Factor Receptor-Like 2



50 30 10 AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAAACTGAGTGGTATCCCCCGGGCCT 110 90 70 GCAGGAATTCCAACCTGCCTGAAGGGACCCTGCCCTGGAACTGACAGTGCAAGCTCGGCG 170 150 130 TCCTGCCCATCTGGGAAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCCAGGACCTTC 230 210 190 290 270 250 TCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTCAGCCTGGCA F SLA G H L V S 0 G M L G S W 330 350 310 GGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCTGGCCTGTGGATGGTGTCCC Α C G W V D Α 410 390 370 GGCCTCCACGTACCCCCTCTCAGCCCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCG S S W Μ G 470 450 430 AGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGC G Н C S ٧ C N C 530 510 490 ATCGTCCAGGACGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGC S A A C R C Q D Н 570 590 550 CAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCGG E S Q D 0 N C P RG Τ RVQKG 650 630 610 N V S Р S K * Ţ R ΡW R Р Μ G S L 710 690 670 CGGGGGAGCCAGCTCTGTGCCCTGGGGAGGGGGCTCCACGTTGCTTCCCTGGGAGATGA 770 750 730 CCGTCTTCTCCAGCAGAAAGGTTGAAGGTCCCACCCTGAGCGGCACCCTGGTCACATGCC 830 810 TGCGTCCAGGAGAGCTGCAGGGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCC 890 870 850 CAGACAAAGCCTCATCAGATCTGAGCTTCCTGGAGGCTCAGGATGGGCCTTCCCAGAAGC 950 930 AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAA 990 1010 TGTCAGGGCCATGGGAGGGCCCCTGGGCTTCAGGGGTTGGGGAAAGTGAACACTCTGCTC

1030		1070
TTTGTCCACCTTCGGGAGGAC	CAACCTTCAAATGCTC	GACCCTGGGCCCCTAACTGACCTGA
1090	1110	1130
GACTTCAGAGCTTCTTGGGAG	GAGCTGGGGTCCCC	CAGCGGAGCCTGGGATGGAGCAGGG
1150	1170	1190
ATGGCTGCCCCAGGGAGGGGG	CGGTGGGGCCTTCC/	ATCCTGCTCTGCCCTCCTCGTCCTC
1210	1230	1250
TGGCCCCAGCTCAGTCCTGTC	CCATCTCCAGCTCTA	ACCATTTGTGGCCCGACACTGGCTC
1270	1290	1310
TCCCTCTACCTTCTGTCCTTC	GTCTGACACTGGTCT	CCCGTGCTCTGGGGTCTCTGCACTG
1330	1350	1370
ATGGCTGCCTCCCGCTTCTC	TCCCCTCTCCCTCTG	CCGTCCTGTCTCCTGTGGCCAGTCT
1390	1410	1430
CTCCTTGTTTCTCTTCTCCT		CCTCCCCATAGCCGAGCTTGGAAAA
1450	1470	1490
	CTCATCCTGGAGCTG	CCACCAGCCCAGCCTCCCTGGGACC 1550
1510	1530	=
		GGCTCCCTGAGGCTGAGTGAACACTG 1610
1570	1590	
		CACTCCCGCAGGTGCAGCTGGCTGGT 1670
1630	· 1650	TOCCTATECTCCTCTTTCTCTCACGGAG
	ACCAGCAGCTCCCAC	TGGGTATGGTGGTTTCTCTCAGGGAG 1730
1690		CTAATCATATGTGTGAAAAGAAGAAA
	1770	1790
1750	1770 AACCTCATCCTCTCC	GTCCAGGTATTGATCCTCCTCCCCCT
	1830	1850
1810	TOOU TOOCACCTCCCCTCT	CCCCGCTGGGGCTGGTGTTTCTGGTG
	1890	1910
1870	ილი ეენეგიცილი	TGAGTCTTTCAAGTACAGCCACGGTA
1930	1950	1970
T330		CAGTAAAATGAACCCGAGAACCTGGA
1990	2010	2030
CTCCAGGGGGCCTGAGC	:AGGCAGGGTCTCCAC	CGATTCGTGTGCTCACAGCGGGAAAAG
2050	2070	2090
ACAGGAGGCAGAAGGTGAG		GGCCCTGCAGGCCCCTCCGGACGTCAC
2110	2130	2150
CACGGTGGCCGTGGAGGAG	GACAATACCCTCATT(CACGGGGGAGGAGCCCAAACCACTGAC
2170	2190	2210
CCACAGACTCTGCACCCC	SACGCCAGAGATACC	TGGAGCGACGGCTGCTGAAAGAGGCTG
2230	2250	22/0
TCCACCTGGCGAAACCAC	CGGAGCCCGGAGGTT	TGGGGGCTCCGCCCTGGGCTGGTTTCC

GTCTCCTCCAGTGGAGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGT GCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCC AGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCACACCCCAGCCCTCCT GGGTCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCT ${\tt CAGCAGGACAGGCCCGGGCACTGCCTTCAAGCCAAGGCTGGACTGGGTTGGCTGCAGTG}$ TGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTTGAAAAAAA

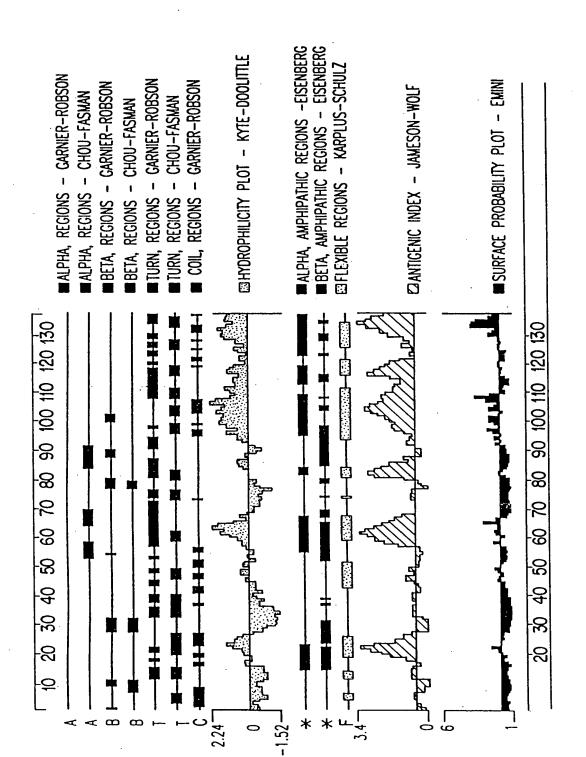
FIG.7C

1	MLGTSGHLVWLSQGFSLAGRPGSSPWPVD	29
1	::.:::::::::::::::::::::::::::::::::::	49
30	AVLACGWC.PGLHVPPLSPSSW	50
50	AQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR	99
51	TPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQR	100
100	CSSDQV.ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFG	148
101	VQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRPSK	136
149	.:. . .: . :. ::: VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA	198

FIG.8

Appl. No. 09/340,690; Group Art Unit: 1647 Dkt. No. 1488.0770007/EKS/PAJ; Batch No.: N/A Inventor(s): Ni et al.; Tel: 202/371-2600

Title: Human Tumor Necrosis Factor Receptor-Like 2



F16.9

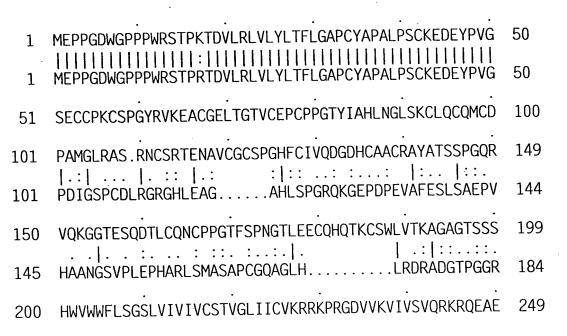


FIG.10

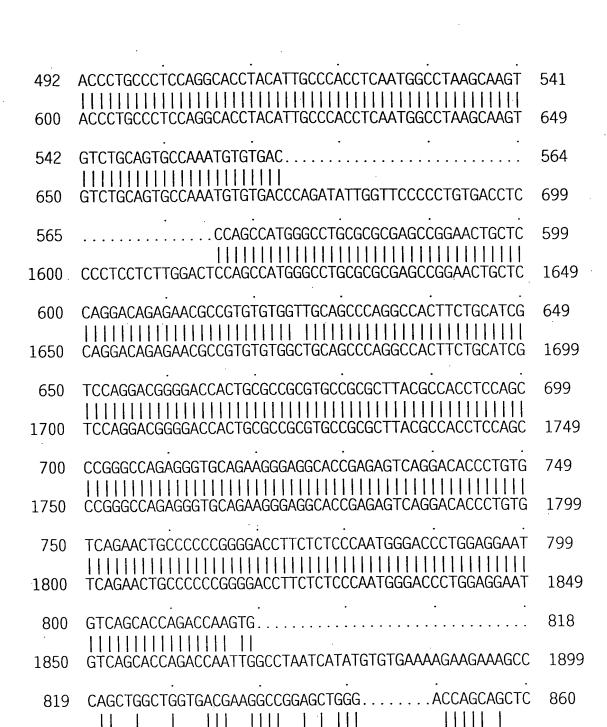
	•	
1	MEPPGDWGPPPWRSTPKTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVG	50
1	:: ::: : :: ::: ::: :::: :::: :::	29
51	SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD	100
30	AVLACGWCPGLHVPPLSPSSWT	51
101	PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRV	150
52		101
151	QKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSSH	200
102		136

FIG.11

1	MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCK	43
1.	MLGTSGHLVWLSQGFSLAGRPGSSPWPVDAVLACGWCP	38
44	EDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKC	93
39	: . . .:: . : .: : .: GLHVPPLSPSSWTPAMGLRASRNCSRTENAVCGCSPGHFCI VQDGDHC	86
94	LQCQMCDPDIGSPCDLRGRGHLEAGAHLSPGRQKGEPDPEVAFESLSAEP	143
87	. .:: .:.: :: .::.: . AACRAYATSSPGQRVQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRP	134
L44	VHAANGSVPLEPHARLSMASAPCGQAGLHLRDRADGTPGGRA. 185	
135	SK 136	

FIG.12

1	GCACGAGCTGCCTCCCGCAGGCGCCACCTGTGTCCCCCAGCG	42
101	TTGCCTGGACAGCTCCTGCCTCAGGCA.GCGCCACCTGTGTCGCCCAGCG	149
43	CCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTG	92
150		199
93	CTGCCCACT.CTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCG	141
200	CTGCCCACTACTCCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCG	249
142	AGGCGGATTCTCTTTCTCTTTCTCTTCTCTGGCCCACAGCCGCAGC	191
250	AGGCGGATTCTCTTTCTCTTTCTCTTCTCTGGCCCACAGCCGCAGC	299
192	AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG	241
300	AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG	349
242	AGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCT	291
350	AGCTGCCGGTCTGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCT	. 399
292	CCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTA	341
400		449
342	TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCA	391
450	TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCA	499
392		441
500		549
442		491
550		599



AAGGGGTGAGCACACGGTGGCCCCATCAGGGTTCATGTCCCCAGCCGTCA

CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT

CCTCTTGGAGCTCTGTCACCCCAAGCCTGGGAGGTGGCCCCAGAGCTTTT

1900

861

1950

1949

910

1999

911	GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT	960
2000		2049
961	GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGG .AAAAGACAGGAGGCAG	1009
2050	TATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAG	2099
1010	AAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACC	1059
2100	AAGGTGAGGCCACAGTCATTGA.GCCCTGCAGGCCCCTCCGGACGTCACC	2148
1060	ACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAA	1109
2149	ACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAA	2198
1110	CCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGAC	1159
2199	CCACTGACCCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGAGAC	2248
1160	GGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGAGCCCGGAGG	1209
2249	GGCTG. CTGATAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGG	2297
1210	CTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAG	1259
2298	CTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCAGTGGAGGGAG	2347
1260	GGTGGCGCCCCTGCTGG GGTAGAGCTGGGGACGCCACGTGCCATTCCCA	1308
2348	GGTGGTGCCCCTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCA	2397
1309	TGGGCCAGTGAGGGCCTGG.GGCCTCTGTTCTGCTGTGGCCTGAGCTCCC	1357
2398		2447
1358	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCACACAC	1407
2448	CAGAGTCCTGAGGAGGAGCCCCAGTTGCCCCTCGCTCACAGACCACACAC	2497

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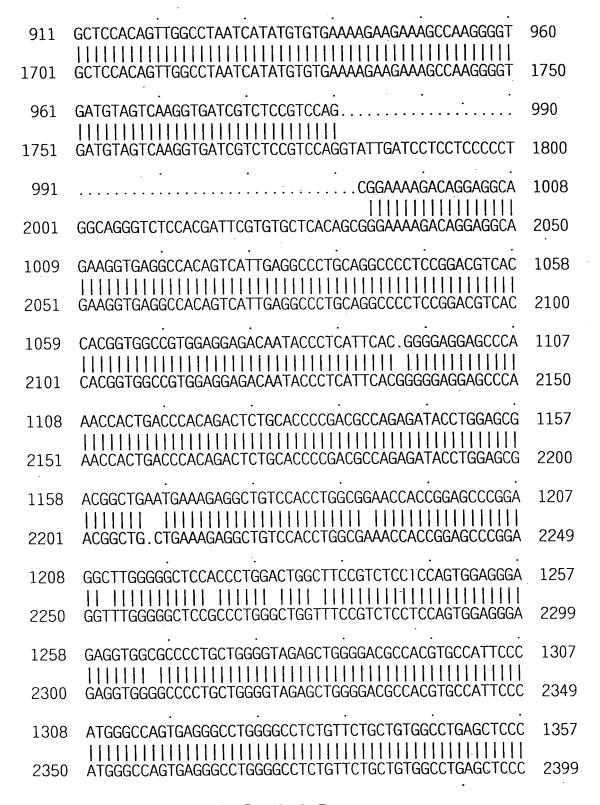
Appl. No. 09/340,690; Group Art Unit: 1647 Dkt. No. 1488.0770007/EKS/PAJ; Batch No.: N/A Inventor(s): Ni et al.; Tel: 202/371-2600 Title: Human Tumor Necrosis Factor Receptor-Like 2

1408	CCAGCCCTCCTGGGCCAACCCAGAGG.GCCTTCAGACCCCAGCTGTGTGC	1456
2498	CCAGCCCTCCTGGGCCAACCCAGAGGCCCCTTCAGACCCCAGCTGTCTGC	2547
1457	GCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCAC	1506
2548	GCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCAC	2597
1507	AGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGTTTAGTGGATACCAC	1556
2598	AGCCAAGGCTGGAATGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCAC	2647
1557	ATCGGAAGTGATTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCT	1604
2648		· 2692

FIG.13D

1	GCACGAGCTGCCTCCCGCAGGCGC	24
701	GTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGCAGAAAGGTTGAAGGTC	750
25	CACCTGTGTCCCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTCT	74
751	CCACCCTGAGCGGCACCCTGGTCACATGCCTGCGTCCAGGAGAGCTGCAG	800
75	GCTGCCAGACACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGG	124
801	GGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCCCAGACAAAGC	850
125	CACAGCTTGTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTC	174
851		900
175	TGGCCCACAGCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTT	219
901	AGGCCCAGAGGGAGGCTGCCCCCAGATCCCCTGTCCCCTGGGGCTGTGGG	950
220	CATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGA	269
951	TGTCCCTGAATGTCAGGGCCATGGGAGGGCCCCTGGGCTTCAGGGGTTGG	1000
270	GCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCCAA	314
1001		1050
315	A ACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGA	357
1051	ATGCTGACCCTGGGCCCCTAACTGACCTGAGACTTCAGAGCTTCTTGGGA	1100
358	GCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCC	407
1101		1150
408	AGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGG	457
1151		1200

458	AGG. CCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCTGCCCTCCAG	505
1201	TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTTGTGGCCCG	1250
506	GCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCC	553
1251	ACACTGGCTCTCCCTCTACCTTCTGTCCTTGTCTGACACTGGTCTCCCGT	1300
554	. AAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCCAG	602
1301	GCTCTGGGGTCTCTGCACTGATGGCTGCCTCCCGCTTCTCCCCTCTCC	1350
603	GACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCC	652
1351	CTCTGCCGTCCTGTCTCCTGTGGCCAGTCTCTCCTTGTTTCTCTTCTCCT	1400
653	AGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCG	702
1401	CCTTCCTCTCCCACCTCCCCATAGCCGAGCTTGGAAAAGTCAGACAGA	1450
703	GGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCA	752
1451	CCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCCAGCC	1500
753	GAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGG	796
1501	TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGA	1550
797		810
1551	GTGAACACTGGGCGCTGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCC	1600
811		860
1601		
861	CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTT	Г 910 I
1651	CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTT	T 1700



1358	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCACACAC	1407
2400	CAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCACACAC	2449
1408	CCAGCCCTCCTGGG.CCAACCCAGAGGG.CCTTCAGACCCCAGCTGTGTG	1455
2450	CCAGCCCTCCTGGGTCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTG	2499
1456	CGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCA	1505
2500		2549
1506	CAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCA	1555
2550		2599
1556	CATCGGAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTA	1605
2600		2637

FIG.14D

1	CCCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGGAGAA	50
1	AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAAACTGAGTGGT	47
51	CTCGCCCCTCCCATCGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCT	100
48	ATCCCCCGGGCCTGCAGG. AATTCCAACCTGCCTGAAGGGACCCTGCCCT	96
101	TTGCCTGGACAGCTCCTGCCTCAGGCAGCGCCACCTGTGTCGCCCAGCGC	150
97	GGAACTGACAGTGCAAGCTCGGCGTCCTGCCCATCTGGGAAGAAGGCT	144
151	CGCTCCACCCAGCAGGCCTGAGCCCCTTCTGCTGCCAGACACCCCCTGC	200
145	GGTTTCTCCCATCAACGAAGCCCTCCCAGGACCTTCCTGCAAGCCCTCGT	194
201	TGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCGA	250
195	CCCACACGCAGCTCTGCCGTCCCTTGGTGTCCCTCCCGGCCTCAGGT	241
251	GGCGGATTCTCTTTCTCTTTCTCTTCTGGCCCA.CAGCCGCAGC	299
242	CCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTC	291
300	AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG	349
292	AGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCT	341
350	AGCTGCCGGTCTGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCT	399
342	GGCCTGTGGATGGTGTCCCGGCCTCCACGTACCCCCTCTCAGCCC	386
400	CCTCCCTGGAGATCCACCCCCAGAACCGACGTCTTGAGGCTGGTGCTGTA	449
387	CTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCCA	436
450	TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCG. TCCTGC	498
437	GGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGCATCGTC	486

499 487	AAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCC	548 536
549	AGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTG	598
537		586
599	AACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG	648
587	AGAACTGCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAATG	634
649	TGTCTGCAGTGCCAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCT	698
635	TCAGCACCAGACCAAGTAAGTGAACCCGGGGGAGGCCAGCTCTGTGCCCT	684
699	CAGGGAAGAGGTCACCTGGAGGCTGGTGCCCACCTGAGTCCAGGCAGAC	748
685	GGGGAGGGGCTCCACGTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGC	734
749	AGAAAGGGGAACCAGACCCAGAGGTGGCCTTTGAGTCACTGAGCG	793
735	AGAAAGGTTGAAGGTCCCACCCTGAGCGGCACCCTGGTCACATGCCTGCG	784
794	CAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCATGCC	843
785	TCCAGGAGAGCTGCAGGGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCA	834
844	AGGCTCAGCATGCCCAGTGCTCCCTGCGGCCAGGCAGGACTGCACCTGCG	893
835	TGGGCCCAGACAAAGCCTCATCAGATCTGAGCTTCCTGGAGGCTCAGGAT	884
894	GGACAGGGCTGACGGCACACCTGGGGGCCTGAGCCTACAGGGAGG	943
885	GGGCCTTCCCAGAAGCAGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGT	934
944	CACAGGGCAGGTGGGCTAGCCATGAACAGAAGAGGAAGCTGGAGTGCTTT	993
935	CCCCTGGGGCTGTGGGTGTCCCTGAATGTCAGGGCCATGGGAGGGCCCCT	984

994		1043
985	GGGCTTCAGGGGTTGGGGAAAGTGAACACTCTGCTCTTTGTCCACCTTCG	1034
1044	TGCCCAGTTCCATGCCCCTCCCCTCTTGTGAAAGCACCTGTCTACTTGGG	1093
1035	GGAGGACAACCTTCAAATGCTGACCCTGGGCCCCTAACTGA	1075
1094	CTGAGGATGTGGGGGCACAGGTGGCAGGTGAGGCTGCCCTCAGGAGGGGC	1143
1076	CCTGAGACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCCAGCGGAGCC	1125
1144	CCAGGCCCAGCTTGTACCCCACCTCCACCAGTACCTGAAGAAGTGGGGCT	1193
1126	TGGGATGGAGCAGGGATGGCTGCCCCAGGGAGGGGGGGGGTGG	1167
1194	CTCACCCTACCTGCCTCTGCCATTGGAATGGCCTGGTTTGCACAGATGGG	1243
1168	GGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTCTGGCCCCAGCTCAGTCC	1217
1244	AAACCCGTTTGAGGGGTGGGTGTCTGGGTGGGCACGTGGGGCGAGGACCT	1293
1218	TGTCCATCTCCAGCTCTAACCATTTGTGGCCCGACACTGGCTCTCCCTCT	1267
1294	GCCTGAGGGACCCTGCCCTGGAACTGACAGTGCAAGCTCGGCGTCCTGCC	1343
1268	ACCTTCTGTCCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCA	1317
1344	CATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCCAGGACC	1393
1318		1367
1394		1443
1368		1417
1444	TCCCGGCCTCAGGTCCTCCATGCTGGGTACCTCTGGGCACCTCGTT	1489
1418		1467

L490	TGGCTGAGCCAGGGGTTCAGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTG	1539
1468	TGGAGCTGCCACCAGCCCAGCCTCCCTGGGACCTGTCTTCACTGCCTGGG	1517
1540	GCCTGTGGATGCTGTCCTGGCCTGTG.GATGGTGTCCCGCCCTCCACGTA	1588
1518	GCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTGGGCGCTG	1567
1589	CCCCTCTCACCCCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCGAGC	1638
1568	CACCTGCCTCTCCCACGTCCTCGGCCCCA	1603
1639	CGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCA	1688
1604	AGGTGCAGCTGGTGACGAAGCCCGGAGCTGGGACCAGCAGCTCCCA	1653
1689	CTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACG	1738
1654	CTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTTGCT	1703
1739	CCACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAG	1788
1704		1753
1789	GACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGG	1835
1754	GTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCTCTC	1803
1836	GACCCTGGAGGAATGTCAGCACCAGACCAATTGGCCTAATCATATGTGTG	1885
1804	cctccccctccAccttcccAcctccccctctccccgctgggctggtgtt	1853
1886	AAAAGAAGAAAGCCAAGGGGTGAGCACACGGTGGCCCCATCAGGGTT	1932
1854		1903
1933	CATGTCCCCAGCCGTCACCTCTTGGAGCTCTGTCACCCCAAGCCTGGGAG	
1904		1947

1983	GTGGCCCCAGAGCTTTTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACT	2032
1948	CTGAAAGCAGTAAAATGAACCCGAGAACCTGGAGTCCCAGGGGGGCCTGA	1997
2033 1998	GCAGGCTGGGGCAGGTGTATGTAGTCAAGGTGATCGTCTCCGTCCAGCGG	2082
2083	TAAAAGACAGGAGGCAGAAGGTGAGGCCACAGTCATTGA . GCCCTGCAGG	2131
2035		2084
2132	CCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAATACCCTCATTC	2181
2085	CCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACAATACCCTCATTC	2134
2182	AC.GGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGCC	2230
2135		2184
2231	AGAGATACCTGGAGAGACGGCTGCTGATAGAGGCTGTCCACCTGGCGAAA	2280
2185	AGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTGTCCACCTGGCGAAA	2234
2281	CCACCGGAGCCCGGAGGCTTGGGGGGCTCCGCCCTGGGCTGGTTTCCGTCT	2330
2235	CCACCGGAGCCCGGAGGTTTGGGGGGCTCCGCCCTGGGCTGGTTTCCGTCT	2284
2331	CCTCCAGTGGAGGGAGAGGTGGTGCCCCTGCTGGTGGTAGAGCTGGGGAC	2380
2285	CCTCCAGTGGAGGAGAGGTGGGGCCCCTGCTGG.GGTAGAGCTGGGGAC	2333
2381	GCCACGTGCCATTCCCATGGTTCAGTGAGGGGCTGGTGGCCTCTGTTCTG	2430
2334	GCCACGTGCCATTCCCATGGGCCAGTGAGGGCCTGG.GGCCTCTGTTCTG	2382
2431	CTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCCCCAGTTGCCCCTC	2480
2383	CTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTC	2432

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Appl. No. 09/340,690; Group Art Unit: 1647 Dkt. No. 1488.0770007/EKS/PAJ; Batch No.: N/A Inventor(s): Ni et al.; Tel: 202/371-2600 Title: Human Tumor Necrosis Factor Receptor-Like 2



FIG.15F

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C PGPGQDTD C R C TKTSDTV C D C TEPTETE C L C DNNRNQI C S C GELTGTV C E	C TVDRDTV C TREQNRI G TSETDTI C SSTSNAE C SRTENAV	C DEKONTV G TETSDVV G VSDTI C KD G TESQDTL	C TKL G NASMDAV G TNKTDVV G TKERDVV G AGTSSSH
C HKGTYLYND C SPGQHAKVF C QPGQKLVSD C PAGTF C SPGYRVKEA	C SSDQVETSS C SSDQVETQA C DPNLGLRVQQK C KGVFRTRKE C DPAMGLRASRN	C FN C SL C LNGTVHLS C QEKQN C RL C APLRK C RPGFGVARP G TETSD C SM C EQD C KQCQELTKKG C KD C AA C RAYAT S SPGQRVQKG G TESQD	C KKSLE C NVVAIP C ETKDLVVQQA C SLDGKSVLVN C SWLVTKA
00000 600000	C C C C C C C C C C C C C C C C C C C	C FN C SL C RL C APLRK C ES C VLHRS C SM C EQD C AA C RAYAT	C RP H QI C RP W TS C RP W TS
V C POCKY I HPONNS I T C RL REYYDOT AQM A C REKOYL INSO - S C KEDEYPVGSE	E C ESGSFTASENHLRH S C EDSTYTQLWNWVPE P C GESEFLDTWNRETH P C PPNSFSSAGGORT P C PPGTYTAHLNGLSK	C RKNQYRHYWSENLFQ C RPGWY C ALSKQEG C EEGWH C TSEA C TPGFH C LGAG C SPGHF C IVQDGDW	- C HAGFFLRENE P C APCTFSNTTSSTDI P C PVGFFSNVSSAFEK - C F-GTFNKQKRGI N C PPGTFSPNGTLEE
TNFR-1 TNFR-11 CD40 · 4-1BB TR-2	TNFR-1 TNFR-11 CD40 4-1BB TR-2	TNFR-1 TNFR-11 CD40 4-1BB TR-2	TNFR-1 TNFR-11 CD40 4-18B TR-2

FIG. 16